*Re-run*
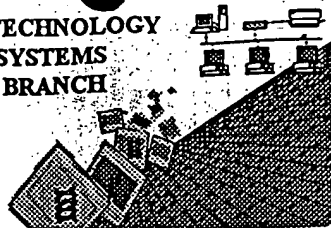
*S. Brader*

# RAW SEQUENCE LISTING
## ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: __09/757,655__
Source: __/600__
Date Processed by STIC: __2/21/2002__ ✗

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE __CHECKER VERSION 3.1 PROGRAM__, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
           http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
           Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

**ERROR DETECTED**          **SUGGESTED CORRECTION**          SERIAL NUMBER: _09/757,655_

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)          SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

160

RAW SEQUENCE LISTING                           DATE: 02/21/2002
PATENT APPLICATION:  US/09/757,655             TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

Does Not Comply
Corrected Diskette Needed

*pp 1-5*

```
 3 <110> APPLICANT: FUJII, Takeru
 4         YOKOYAMA, Hideakira
 5         HAMAMOTO, Hidetoshi
 7 <120> TITLE OF INVENTION: A PEPTIDE HAVING AN AFFINITY FOR gp120
 9 <130> FILE REFERENCE: 2001-0019A/LC/01732
11 <140> CURRENT APPLICATION NUMBER: 09/757,655
12 <141> CURRENT FILING DATE: 2001-01-11
14 <150> PRIOR APPLICATION NUMBER: JP No. 2000-6182
15 <151> PRIOR FILING DATE: 2000-01-11
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 5
23 <212> TYPE: PRT
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
29 <220> FEATURE:
30 <221> NAME/KEY: Residue
31 <222> LOCATION: (1)
32 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr
34 <220> FEATURE:
35 <221> NAME/KEY: Residue
36 <222> LOCATION: (2)
37 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
39 <220> FEATURE:
40 <221> NAME/KEY: Residue
41 <222> LOCATION: (3)
42 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
44 <220> FEATURE:
45 <221> NAME/KEY: Residue
46 <222> LOCATION: (4)
47 <223> OTHER INFORMATION: Xaa = Ala, Trp or Gly
49 <220> FEATURE:
50 <221> NAME/KEY: Residue
51 <222> LOCATION: (5)
52 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
53         Phe, Trp, Pro or Tyr
55 <400> SEQUENCE: 1
56 Xaa Xaa Xaa Xaa Xaa
57  1               5
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 5
```

W--> 30
W--> 35
W--> 40
W--> 45
W--> 50

*insufficient explanation give source of genetic material (see item on Error Summary Sheet)*

(Peptide)

```
         61 <212> TYPE: PRT
         62 <213> ORGANISM: Artificial Sequence
         64 <220> FEATURE:
         65 <223> OTHER INFORMATION: Description of Artificial Sequence:(Peptide)
         67 <220> FEATURE:
W--> 68 <221> NAME/KEY: Residue
         69 <222> LOCATION: (1)
         70 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr, or polypeptide
residue that an
         71        arbitrary amino acid stood in line in the N-terminal side from this amino acid
         73 <220> FEATURE:
W--> 74 <221> NAME/KEY: Residue
         75 <222> LOCATION: (2)
         76 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
         78 <220> FEATURE:
W--> 79 <221> NAME/KEY: Residue
         80 <222> LOCATION: (3)
         81 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
         83 <220> FEATURE:
W--> 84 <221> NAME/KEY: Residue
         85 <222> LOCATION: (4)
         86 <223> OTHER INFORMATION: Xaa = Ala, Trp or Gly
         88 <220> FEATURE:
W--> 89 <221> NAME/KEY: Residue
         90 <222> LOCATION: (5)
         91 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His
Lys, Arg,
         92        Phe, Trp, Pro or Tyr
         94 <400> SEQUENCE: 2
W--> 95 Xaa Xaa Xaa Xaa Xaa
         96  1                  5
         98 <210> SEQ ID NO: 3
         99 <211> LENGTH: 5
        100 <212> TYPE: PRT
        101 <213> ORGANISM: Artificial Sequence
        103 <220> FEATURE:
        104 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
        106 <220> FEATURE:
W--> 107 <221> NAME/KEY: Residue
        108 <222> LOCATION: (1)
        109 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr
        111 <220> FEATURE:
W--> 112 <221> NAME/KEY: Residue
        113 <222> LOCATION: (2)
        114 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
        116 <220> FEATURE:
W--> 117 <221> NAME/KEY: Residue
        118 <222> LOCATION: (3)
        119 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
        121 <220> FEATURE:
W--> 122 <221> NAME/KEY: Residue
```

RAW SEQUENCE LISTING       DATE: 02/21/2002
PATENT APPLICATION: US/09/757,655      TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

```
       123 <222> LOCATION: (4)
       124 <223> OTHER INFORMATION: Xaa = Ala, Trp or Gly
       126 <220> FEATURE:
W--> 127 <221> NAME/KEY: Residue
       128 <222> LOCATION: (5)
       129 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Thr, Met, Asn, Gln, His, Lys,
Arg,
       130        Phe, Trp, Pro or Tyr, or polypeptide residue that an arbitrary amino acid
       131        stood in line in the C-terminal side of this amino acid, H
       133 <400> SEQUENCE: 3
       134 Xaa Xaa Xaa Xaa Xaa
       135   1               5
       138 <210> SEQ ID NO: 4
       139 <211> LENGTH: 5
       140 <212> TYPE: PRT
       141 <213> ORGANISM: Artificial Sequence
       143 <220> FEATURE:
       144 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
       146 <220> FEATURE:
W--> 147 <221> NAME/KEY: Residue
       148 <222> LOCATION: (1)
       149 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp
       151 <220> FEATURE:
W--> 152 <221> NAME/KEY: Residue
       153 <222> LOCATION: (2)
       154 <223> OTHER INFORMATION: Xaa = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys
       156 <220> FEATURE:
W--> 157 <221> NAME/KEY: Residue
       158 <222> LOCATION: (3)
       159 <223> OTHER INFORMATION: Xaa = Lys, Tyr, Arg, Glu, Met or Trp
       161 <220> FEATURE:
W--> 162 <221> NAME/KEY: Residue
       163 <222> LOCATION: (4)
       164 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
       165        Phe or Trp
       167 <220> FEATURE:
W--> 168 <221> NAME/KEY: Residue
       169 <222> LOCATION: (5)
       170 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
       171        Phe, Tyr or Trp
       173 <400> SEQUENCE: 4
       174 Xaa Xaa Xaa Xaa Xaa
       175   1               5
       177 <210> SEQ ID NO: 5
       178 <211> LENGTH: 5
       179 <212> TYPE: PRT
       180 <213> ORGANISM: Artificial Sequence
       182 <220> FEATURE:
       183 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
       185 <220> FEATURE:
```

```
W--> 186 <221> NAME/KEY: Residue
     187 <222> LOCATION: (1)
     188 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp, or polypeptide
residue that an
     189         arbitrary amino acid stood in the N-terminal side from this amino acid
     191 <220> FEATURE:
W--> 192 <221> NAME/KEY: Residue
     193 <222> LOCATION: (2)
     194 <223> OTHER INFORMATION: Xaa = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys
     196 <220> FEATURE:
W--> 197 <221> NAME/KEY: Residue
     198 <222> LOCATION: (3)
     199 <223> OTHER INFORMATION: Xaa = Lys, Tyr, Arg, Glu, Met or Trp
     201 <220> FEATURE:
W--> 202 <221> NAME/KEY: Residue
     203 <222> LOCATION: (4)
     204 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
     205         Phe or Trp
     207 <220> FEATURE:
W--> 208 <221> NAME/KEY: Residue
     209 <222> LOCATION: (5)
     210 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
     211         Phe, Tyr or Trp
     213 <400> SEQUENCE: 5
     214 Xaa Xaa Xaa Xaa Xaa
     215  1                 5
     217 <210> SEQ ID NO: 6
     218 <211> LENGTH: 5
     219 <212> TYPE: PRT
     220 <213> ORGANISM: Artificial Sequence
     222 <220> FEATURE:
     223 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     225 <220> FEATURE:
W--> 226 <221> NAME/KEY: Residue
     227 <222> LOCATION: (1)
     228 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp
     230 <220> FEATURE:
W--> 231 <221> NAME/KEY: Residue
     232 <222> LOCATION: (2)
     233 <223> OTHER INFORMATION: Xaa = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys
     235 <220> FEATURE:
W--> 236 <221> NAME/KEY: Residue
     237 <222> LOCATION: (3)
     238 <223> OTHER INFORMATION: Xaa = Lys, Tyr, Arg, Glu, Met or Trp
     240 <220> FEATURE:
W--> 241 <221> NAME/KEY: Residue
     242 <222> LOCATION: (4)
     243 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
     244         Phe or Trp
     246 <220> FEATURE:
```

```
W--> 247 <221> NAME/KEY: Residue
     248 <222> LOCATION: (5)
     249 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
     250         Phe, Tyr or Trp, or polypeptide residue that an arbitrary amino acid stood in
line
     251         in the C-terminal side of this amino acid
     253 <400> SEQUENCE: 6 /
W--> 254 Xaa Xaa Xaa Xaa Xaa
     255   1           5
     257 <210> SEQ ID NO: 7
     258 <211> LENGTH: 7
     259 <212> TYPE: PRT
     260 <213> ORGANISM: Artificial Sequence
     262 <220> FEATURE:
     263 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     265 <400> SEQUENCE: 7
     266 Gly Gly Asp Val Lys Ala Gly
     267   1           5
     269 <210> SEQ ID NO: 8
     270 <211> LENGTH: 6
     271 <212> TYPE: PRT
     272 <213> ORGANISM: Artificial Sequence
     274 <220> FEATURE:
     275 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     277 <400> SEQUENCE: 8
     278 Gly Asp Val Lys Ala Gly
     279   1           5
     281 <210> SEQ ID NO: 9
     282 <211> LENGTH: 6
     283 <212> TYPE: PRT
     284 <213> ORGANISM: Artificial Sequence
     286 <220> FEATURE:
     287 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     289 <400> SEQUENCE: 9
     290 Gly Tyr Tyr Lys Ala Ala
     291   1           5
     293 <210> SEQ ID NO: 10
     294 <211> LENGTH: 6
     295 <212> TYPE: PRT
     296 <213> ORGANISM: Artificial Sequence
     298 <220> FEATURE:
     299 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
     301 <400> SEQUENCE: 10
     302 Gly Tyr Ala Tyr Arg Lys
     303   1           5
     305 <210> SEQ ID NO: 11
     306 <211> LENGTH: 6
     307 <212> TYPE: PRT
     308 <213> ORGANISM: Artificial Sequence
     310 <220> FEATURE:
```

*Please correct this error in subsequent sequences*

**VERIFICATION SUMMARY**
PATENT APPLICATION:  US/09/757,655

DATE: 02/21/2002
TIME: 11:38:42

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

```
L:30 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:35 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:40 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:45 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:50 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:68 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:74 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:79 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:84 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:89 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:112 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:117 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:122 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:127 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:152 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:157 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:168 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:186 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:197 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:202 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:208 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:226 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:231 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:236 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:241 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:247 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
```